Figure 1:
WWP1 open reading frame and translation to corresponding polypeptide

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1     ATG GCC ACT GCT TCA CCA AGG TCT GAT ACT AGT AAT AAC CAC AGT   45
1      M   A   T   A   S   P   R   S   D   T   S   N   N   H   S    15

46    GGA AGG TTG CAG TTA CAG GTA ACT GTT TCT AGT GCC AAA CTT AAA   90
16     G   R   L   Q   L   Q   V   T   V   S   S   A   K   L   K    30

91    AGA AAA AAG AAC TGG TTC GGA ACA GCA ATA TAT ACA GAA GTA GTT   135
31     R   K   K   N   W   F   G   T   A   I   Y   T   E   V   V    45

136   GTA GAT GGA GAA ATT ACG AAA ACA GCA AAA TCC AGT AGT TCT TCT   180
46     V   D   G   E   I   T   K   T   A   K   S   S   S   S   S    60

181   AAT CCA AAA TGG GAT GAA CAG CTA ACT GTA AAT GTT ACG CCA CAG   225
61     N   P   K   W   D   E   Q   L   T   V   N   V   T   P   Q    75

226   ACT ACA TTG GAA TTT CAA GTT TGG AGC CAT CGC ACT TTA AAA GCA   270
76     T   T   L   E   F   Q   V   W   S   H   R   T   L   K   A    90

271   GAT GCT TTA TTA GGA AAA GCA ACG ATA GAT TTG AAA CAA GCT CTG   315
91     D   A   L   L   G   K   A   T   I   D   L   K   Q   A   L   105

316   TTG ATA CAC AAT AGA AAA TTG GAA AGA GTG AAA GAA CAA TTA AAA   360
106    L   I   H   N   R   K   L   E   R   V   K   E   Q   L   K   120

361   CTT TCC TTG GAA AAC AAG AAT GGC ATA GCA CAA ACT GGT GAA TTG   405
121    L   S   L   E   N   K   N   G   I   A   Q   T   G   E   L   135

406   ACA GTT GTG CTT GAT GGA TTG GTG ATT GAG CAA GAA AAT ATA ACA   450
136    T   V   V   L   D   G   L   V   I   E   Q   E   N   I   T   150

451   AAC TGC AGC TCA TCT CCA ACC ATA GAA ATA CAG GAA AAT GGT GAT   495
151    N   C   S   S   S   P   T   I   E   I   Q   E   N   G   D   165

496   GCC TTA CAT GAA AAT GGA GAG CCT TCA GCA AGG ACA ACT GCC AGG   540
166    A   L   H   E   N   G   E   P   S   A   R   T   T   A   R   180

541   TTG GCT GTT GAA GGC ACG AAT GGA ATA GAT AAT CAT GTA CCT ACA   585
181    L   A   V   E   G   T   N   G   I   D   N   H   V   P   T   195

586   AGC ACT CTA GTC CAA AAC TCA TGC TGC TCG TAT GTA GTT AAT GGA   630
196    S   T   L   V   Q   N   S   C   C   S   Y   V   V   N   G   210

631   GAC AAC ACA CCT TCA TCT CCG TCT CAG GTT GCT GCC AGA CCC AAA   675
211    D   N   T   P   S   S   P   S   Q   V   A   A   R   P   K   225

676   AAT ACA CCA GCT CCA AAA CCA CTC GCA TCT GAG CCT GCC GAT GAC   720
226    N   T   P   A   P   K   P   L   A   S   E   P   A   D   D   240

721   ACT GTT AAT GGA GAA TCA TCC TCA TTT GCA CCA ACT GAT AAT GCG   765
241    T   V   N   G   E   S   S   S   F   A   P   T   D   N   A   255

766   TCT GTC ACG GGT ACT CCA GTA GTG TCT GAA GAA AAT GCC TTG TCT   810
256    S   V   T   G   T   P   V   V   S   E   E   N   A   L   S   270

811   CCA AAT TGC ACT AGT ACT ACT GTT GAA GAT CCT CCA GTT CAA GAA   855
271    P   N   C   T   S   T   T   V   E   D   P   P   V   Q   E   285

856   ATA CTG ACT TCC TCA GAA AAC AAT GAA TGT ATT CCT TCT ACC AGT   900
286    I   L   T   S   S   E   N   N   E   C   I   P   S   T   S   300

901   GCA GAA TTG GAA TCT GAA GCT AGA AGT ATA TTA GAG CCT GAC ACC   945
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301    A   E   L   E   S   E   A   R   S   I   L   E   P   D   T    315

946   TCT AAT TCT AGA AGT AGT TCT GCT TTT GAA GCA GCC AAA TCA AGA    990
316    S   N   S   R   S   S   S   A   F   E   A   A   K   S   R    330

991   CAG CCA GAT GGG TGT ATG GAT CCT GTA CGG CAG CAG TCT GGG AAT   1035
331    Q   P   D   G   C   M   D   P   V   R   Q   Q   S   G   N    345

1036  GCC AAC ACA GAA ACC TTG CCA TCA GGG TGG GAA CAA AGA AAA GAT   1080
346    A   N   T   E   T   L   P   S   G   W   E   Q   R   K   D    360

1081  CCT CAT GGT AGA ACC TAT TAT GTG GAT CAT AAT ACT CGA ACT ACC   1125
361    P   H   G   R   T   Y   Y   V   D   H   N   T   R   T   T    375

1126  ACA TGG GAG AGA CCA CAA CCT TTA CCT CCA GGT TGG GAA AGA AGA   1170
376    T   W   E   R   P   Q   P   L   P   P   G   W   E   R   R    390

1171  GTT GAT GAT CGT AGA AGA GTT TAT TAT GTG GAT CAT AAC ACC AGA   1215
391    V   D   D   R   R   R   V   Y   Y   V   D   H   N   T   R    405

1216  ACA ACA ACG TGG CAG CGG CCT ACC ATG GAA TCT GTC CGA AAT TTT   1260
406    T   T   T   W   Q   R   P   T   M   E   S   V   R   N   F    420

1261  GAA CAG TGG CAA TCT CAG CGG AAC CAA TTG CAG GGA GCT ATG CAA   1305
421    E   Q   W   Q   S   Q   R   N   Q   L   Q   G   A   M   Q    435

1306  CAG TTT AAC CAA CGA TAC CTC TAT TCG GCT TCA ATG TTA GCT GCA   1350
436    Q   F   N   Q   R   Y   L   Y   S   A   S   M   L   A   A    450

1351  GAA AAT GAC CCT TAT GGA CCT TTG CCA CCA GGC TGG GAA AAA AGA   1395
451    E   N   D   P   Y   G   P   L   P   P   G   W   E   K   R    465

1396  GTG GAT TCA ACA GAC AGG GTT TAC TTT GTG AAT CAT AAC ACA AAA   1440
466    V   D   S   T   D   R   V   Y   F   V   N   H   N   T   K    480

1441  ACA ACC CAG TGG GAA GAT CCA AGA ACT CAA GGC TTA CAG AAT GAA   1485
481    T   T   Q   W   E   D   P   R   T   Q   G   L   Q   N   E    495

1486  GAA CCC CTG CCA GAA GGC TGG GAA ATT AGA TAT ACT CGT GAA GGT   1530
496    E   P   L   P   E   G   W   E   I   R   Y   T   R   E   G    510

1531  GTA AGG TAC TTT GTT GAT CAT AAC ACA AGA ACA ACA ACA TTC AAA   1575
511    V   R   Y   F   V   D   H   N   T   R   T   T   T   F   K    525

1576  GAT CCT CGC AAT GGG AAG TCA TCT GTA ACT AAA GGT GGT CCA CAA   1620
526    D   P   R   N   G   K   S   S   V   T   K   G   G   P   Q    540

1621  ATT GCT TAT GAA CGC GGC TTT AGG TGG AAG CTT GCT CAC TTC CGT   1665
541    I   A   Y   E   R   G   F   R   W   K   L   A   H   F   R    555

1666  TAT TTG TGC CAG TCT AAT GCA CTA CCT AGT CAT GTA AAG ATC AAT   1710
556    Y   L   C   Q   S   N   A   L   P   S   H   V   K   I   N    570

1711  GTG TCC CGG CAG ACA TTG TTT GAA GAT TCC TTC CAA CAG ATT ATG   1755
571    V   S   R   Q   T   L   F   E   D   S   F   Q   Q   I   M    585

1756  GCA TTA AAA CCC TAT GAC TTG AGG AGG CGC TTA TAT GTA ATA TTT   1800
586    A   L   K   P   Y   D   L   R   R   R   L   Y   V   I   F    600

1801  AGA GGA GAA GAA GGA CTT GAT TAT GGT GGC CTA GCG AGA GAA TGG   1845
601    R   G   E   E   G   L   D   Y   G   G   L   A   R   E   W    615

1846  TTT TTC TTG CTT TCA CAT GAA GTT TTG AAC CCA ATG TAT TGC TTA   1890
616    F   F   L   L   S   H   E   V   L   N   P   M   Y   C   L    630
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1891  TTT GAG TAT GCG GGC AAG AAC AAC TAT TGT CTG CAG ATA AAT CCA  1935
631    F   E   Y   A   G   K   N   N   Y   C   L   Q   I   N   P   645

1936  GCA TCA ACC ATT AAT CCA GAC CAT CTT TCA TAC TTC TGT TTC ATT  1980
646    A   S   T   I   N   P   D   H   L   S   Y   F   C   F   I   660

1981  GGT CGT TTT ATT GCC ATG GCA CTA TTT CAT GGA AAG TTT ATC GAT  2025
661    G   R   F   I   A   M   A   L   F   H   G   K   F   I   D   675

2026  ACT GGT TTC TCT TTA CCA TTC TAC AAG CGT ATG TTA AGT AAA AAA  2070
676    T   G   F   S   L   P   F   Y   K   R   M   L   S   K   K   690

2071  CTT ACT ATT AAG GAT TTG GAA TCT ATT GAT ACT GAA TTT TAT AAC  2115
691    L   T   I   K   D   L   E   S   I   D   T   E   F   Y   N   705

2116  TCC CTT ATC TGG ATA AGA GAT AAC AAC ATT GAA GAA TGT GGC TTA  2160
706    S   L   I   W   I   R   D   N   N   I   E   E   C   G   L   720

2161  GAA ATG TAC TTT TCT GTT GAC ATG GAG ATT TTG GGA AAA GTT ACT  2205
721    E   M   Y   F   S   V   D   M   E   I   L   G   K   V   T   735

2206  TCA CAT GAC CTG AAG TTG GGA GGT TCC AAT ATT CTG GTG ACT GAG  2250
736    S   H   D   L   K   L   G   G   S   N   I   L   V   T   E   750

2251  GAG AAC AAA GAT GAA TAT ATT GGT TTA ATG ACA GAA TGG CGT TTT  2295
751    E   N   K   D   E   Y   I   G   L   M   T   E   W   R   F   765

2296  TCT CGA GGA GTA CAA GAA CAG ACC AAA GCT TTC CTT GAT GGT TTT  2340
766    S   R   G   V   Q   E   Q   T   K   A   F   L   D   G   F   780

2341  AAT GAA GTT GTT CCT CTT CAG TGG CTA CAG TAC TTC GAT GAA AAA  2385
781    N   E   V   V   P   L   Q   W   L   Q   Y   F   D   E   K   795

2386  GAA TTA GAG GTT ATG TTG TGT GGC ATG CAG GAG GTT GAC TTG GCA  2430
796    E   L   E   V   M   L   C   G   M   Q   E   V   D   L   A   810

2431  GAT TGG CAG AGA AAT ACT GTT TAT CGA CAT TAT ACA AGA AAC AGC  2475
811    D   W   Q   R   N   T   V   Y   R   H   Y   T   R   N   S   825

2476  AAG CAA ATC ATT TGG TTT TGG CAG TTT GTG AAA GAG ACA GAC AAT  2520
826    K   Q   I   I   W   F   W   Q   F   V   K   E   T   D   N   840

2521  GAA GTA AGA ATG CGA CTA TTG CAG TTC GTC ACT GGA ACC TGC CGT  2565
841    E   V   R   M   R   L   L   Q   F   V   T   G   T   C   R   855

2566  TTA CCT CTA GGA GGA TTT GCT GAG CTC ATG GGA AGT AAT GGG CCT  2610
856    L   P   L   G   G   F   A   E   L   M   G   S   N   G   P   870

2611  CAA AAG TTT TGC ATT GAA AAA GTT GGC AAA GAC ACT TGG TTA CCA  2655
871    Q   K   F   C   I   E   K   V   G   K   D   T   W   L   P   885

2656  AGA AGC CAT ACA TGT TTT AAT CGC TTG GAT CTA CCA CCA TAT AAG  2700
886    R   S   H   T   C   F   N   R   L   D   L   P   P   Y   K   900

2701  AGT TAT GAA CAA CTA AAG GAA AAA CTT CTT TTT GCA ATA GAA GAG  2745
901    S   Y   E   Q   L   K   E   K   L   L   F   A   I   E   E   915

2746  ACA GAG GGA TTT GGA CAA GAA GAT TAC AAG GAC GAC GAC GAT AAG  2790
916    T   E   G   F   G   Q   E   D   Y   K   D   D   D   D   K   930

2791  TGA   2793
931    *
```

Figure 2:
WWP1 antisense fragment

CCGCCGCGTTNTAAGCATTTGTGGACCCCTTTAGTNCAGATGACTTCCCATTGCGAGGATCTTTGAATGTTG
TTGTTCTTGTGTTATGATCAACAAAGTACCTTACACCTTCACGAGTATATCTAATTTCCCAGCCTTCTGGCA
GGGGTTCTTCATTCTGTAAGCCTTGAGTTCTTGGATCTTCCCACTGGGTTGTTTTTGTGTTATGATTCACAA
AGTAAACCCTGTCTGTTGAATCCACTCTTTTTTCCCAGCCTGGTGGCAAAGGTCCATAAGGGTCATTTTCTG
CAGCTAACATTGAAGCCGAATAGAGGTATCGTTGGTTAAACTGTTGCATAGCTCCCTGCAATTGGTTCCGCT
GAGATTGCCACTGNTCAAAATTNCGGACAGATTCCATGGTAGGCCGCTGCCACGTTGTTGTTCTGGTGTTAT
GATCCACATAATAAACTCCTCTACGATCATCAACTCTTCTTTCCCAACCTGGAGGTAAAGGTTGTGGTCTCT
CCCATGTGGTAGTTCGAGCATTATGANCCACATAATACGCTCTACCATGAGGATCTTTTCTTTGTTCCCACC
CCTGATGGCAANGNTTCTGTGTTGGCATTCCCAGACTGCTGCCGNACA

Figure 3:
Alignment between the WWP1 open reading frame and the WWP1 antisense fragment of Figure 2

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WWP1 ORF   1    ATGGCCACTGCTTCACCAAGGTCTGATACTAGTAATAACCACAGTGGAAGGTTGCAGTTA
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   61   CAGGTAACTGTTTCTAGTGCCAAACTTAAAAGAAAAAAGAACTGGTTCGGAACAGCAATA
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   121  TATACAGAAGTAGTTGTAGATGGAGAAATTACGAAAACAGCAAAATCCAGTAGTTCTTCT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   181  AATCCAAAATGGGATGAACAGCTAACTGTAAATGTTACGCCACAGACTACATTGGAATTT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   241  CAAGTTTGGAGCCATCGCACTTTAAAAGCAGATGCTTTATTAGGAAAAGCAACGATAGAT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   301  TTGAAACAAGCTCTGTTGATACACAATAGAAAATTGGAAAGAGTGAAAGAACAATTAAAA
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   361  CTTTCCTTGGAAAACAAGAATGGCATAGCACAAACTGGTGAATTGACAGTTGTGCTTGAT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   421  GGATTGGTGATTGAGCAAGAAAATATAACAAACTGCAGCTCATCTCCAACCATAGAAATA
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   481  CAGGAAAATGGTGATGCCTTACATGAAAATGGAGAGCCTTCAGCAAGGACAACTGCCAGG
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   541  TTGGCTGTTGAAGGCACGAATGGAATAGATAATCATGTACCTACAAGCACTCTAGTCCAA
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   601  AACTCATGCTGCTCGTATGTAGTTAATGGAGACAACACACCTTCATCTCCGTCTCAGGTT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   661  GCTGCCAGACCCAAAAATACACCAGCTCCAAAACCACTCGCATCTGAGCCTGCCGATGAC
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   721  ACTGTTAATGGAGAATCATCCTCATTTGCACCAACTGATAATGCGTCTGTCACGGGTACT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   781  CCAGTAGTGTCTGAAGAAAATGCCTTGTCTCCAAATTGCACTAGTACTACTGTTGAAGAT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   841  CCTCCAGTTCAAGAAATACTGACTTCCTCAGAAAACAATGAATGTATTCCTTCTACCAGT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   901  GCAGAATTGGAATCTGAAGCTAGAAGTATATTAGAGCCTGACACCTCTAATTCTAGAAGT
WWP1 AS    1    ------------------------------------------------------------

WWP1 ORF   961  AGTTCTGCTTTTGAAGCAGCCAAATCAAGACAGCCAGATGGGTGTATGGATCCTGTACGG
WWP1 AS    1    ----------------------------------------------------TGTNCGG

WWP1 ORF   1021 CAGCAGTCTGGGAATGCCAACACAGAAACCTTGCCATCA-GGGTGGGAACAAAGAAAAGA
WWP1 AS    8    CAGCAGTCTGGGAATGCCAACACAGAANCNTTGCCATCAGGGGTGGGAACAAAGAAAAGA

WWP1 ORF   1080 TCCTCATGGTAGAACCTATTATGTGGATCATAATACTCGAACTACCACATGGGAGAGACC
WWP1 AS    68   TCCTCATGGTAGAGCGTATTATGTGGNTCATAATGCTCGAACTACCACATGGGAGAGACC

WWP1 ORF   1140 ACAACCTTTACCTCCAGGTTGGGAAAGAAGAGTTGATGATCGTAGAAGAGTTTATTATGT
WWP1 AS    128  ACAACCTTTACCTCCAGGTTGGGAAAGAAGAGTTGATGATCGTAGAGGAGTTTATTATGT
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WWP1 ORF  1200 GGATCATAACACCAGAACAACAACGTGGCAGCGGCCTACCATGGAATCTGTCCGAAATTT
WWP1 AS   188  GGATCATAACACCAGAACAACAACGTGGCAGCGGCCTACCATGGAATCTGTCCGNAATTT

WWP1 ORF  1260 TGAACAGTGGCAATCTCAGCGGAACCAATTGCAGGGAGCTATGCAACAGTTTAACCAACG
WWP1 AS   248  TGANCAGTGGCAATCTCAGCGGAACCAATTGCAGGGAGCTATGCAACAGTTTAACCAACG

WWP1 ORF  1320 ATACCTCTATTCGGCTTCAATGTTAGCTGCAGAAAATGACCCTTATGGACCTTTGCCACC
WWP1 AS   308  ATACCTCTATTCGGCTTCAATGTTAGCTGCAGAAAATGACCCTTATGGACCTTTGCCACC

WWP1 ORF  1380 AGGCTGGGAAAAAAGAGTGGATTCAACAGACAGGGTTTACTTTGTGAATCATAACACAAA
WWP1 AS   368  AGGCTGGGAAAAAAGAGTGGATTCAACAGACAGGGTTTACTTTGTGAATCATAACACAAA

WWP1 ORF  1440 AACAACCCAGTGGGAAGATCCAAGAACTCAAGGCTTACAGAATGAAGAACCCCTGCCAGA
WWP1 AS   428  AACAACCCAGTGGGAAGATCCAAGAACTCAAGGCTTACAGAATGAAGAACCCCTGCCAGA

WWP1 ORF  1500 AGGCTGGGAAATTAGATATACTCGTGAAGGTGTAAGGTACTTTGTTGATCATAACACAAG
WWP1 AS   488  AGGCTGGGAAATTAGATATACTCGTGAAGGTGTAAGGTACTTTGTTGATCATAACACAAG

WWP1 ORF  1560 AACAACAACATTCAAAGATCCTCGCAATGGGAAGTCATCTGTAACTAAAGGTGGTCCACA
WWP1 AS   548  AACAACAACATTCAAAGATCCTCGCAATGGGAAGTCATCTG-NACTAAAGG-GGTCCACA

WWP1 ORF  1620 AATTGCTTATGAACGCGGCTTTAGGTGGAAGCTTGCTCACTTCCGTTATTTGTGCCAGTC
WWP1 AS   606  AA-TGCTTA-NAACGCGGCGG----------------------------------------

WWP1 ORF  1680 TAATGCACTACCTAGTCATGTAAAGATCAATGTGTCCCGGCAGACATTGTTTGAAGATTC
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  1740 CTTCCAACAGATTATGGCATTAAAACCCTATGACTTGAGGAGGCGCTTATATGTAATATT
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  1800 TAGAGGAGAAGAAGGACTTGATTATGGTGGCCTAGCGAGAGAATGGTTTTTCTTGCTTTC
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  1860 ACATGAAGTTTTGAACCCAATGTATTGCTTATTTGAGTATGCGGGCAAGAACAACTATTG
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  1920 TCTGCAGATAAATCCAGCATCAACCATTAATCCAGACCATCTTTCATACTTCTGTTTCAT
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  1980 TGGTCGTTTTATTGCCATGGCACTATTTCATGGAAAGTTTATCGATACTGGTTTCTCTTT
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  2040 ACCATTCTACAAGCGTATGTTAAGTAAAAAACTTACTATTAAGGATTTGGAATCTATTGA
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  2100 TACTGAATTTTATAACTCCCTTATCTGGATAAGAGATAACAACATTGAAGAATGTGGCTT
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  2160 AGAAATGTACTTTTCTGTTGACATGGAGATTTTGGGAAAAGTTACTTCACATGACCTGAA
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  2220 GTTGGGAGGTTCCAATATTCTGGTGACTGAGGAGAACAAAGATGAATATATTGGTTTAAT
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  2280 GACAGAATGGCGTTTTTCTCGAGGAGTACAAGAACAGACCAAAGCTTTCCTTGATGGTTT
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  2340 TAATGAAGTTGTTCCTCTTCAGTGGCTACAGTACTTCGATGAAAAAGAATTAGAGGTTAT
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  2400 GTTGTGTGGCATGCAGGAGGTTGACTTGGCAGATTGGCAGAGAAATACTGTTTATCGACA
WWP1 AS   624  ------------------------------------------------------------

WWP1 ORF  2460 TTATACAAGAAACAGCAAGCAAATCATTTGGTTTTGGCAGTTTGTGAAAGAGACAGACAA
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WWP1 AS    624  ------------------------------------------------------------

WWP1 ORF  2520 TGAAGTAAGAATGCGACTATTGCAGTTCGTCACTGGAACCTGCCGTTTACCTCTAGGAGG
WWP1 AS    624  ------------------------------------------------------------

WWP1 ORF  2580 ATTTGCTGAGCTCATGGGAAGTAATGGGCCTCAAAAGTTTTGCATTGAAAAAGTTGGCAA
WWP1 AS    624  ------------------------------------------------------------

WWP1 ORF  2640 AGACACTTGGTTACCAAGAAGCCATACATGTTTTAATCGCTTGGATCTACCACCATATAA
WWP1 AS    624  ------------------------------------------------------------

WWP1 ORF  2700 GAGTTATGAACAACTAAAGGAAAAACTTCTTTTTGCAATAGAAGAGACAGAGGGATTTGG
WWP1 AS    624  ------------------------------------------------------------

WWP1 ORF  2760 ACAAGAAGATTACAAGGACGACGACGATAAGTGA

WWP1 AS    624  ----------------------------------
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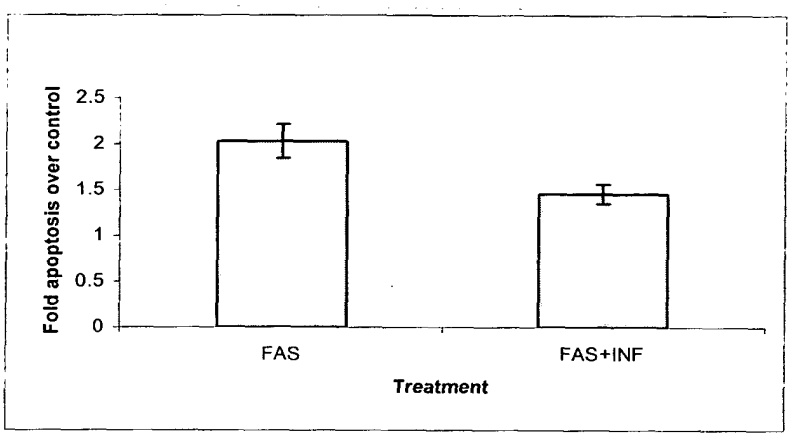
Figure 4:
validation of the anti-apoptotic effect of WWP1

a)



b)